Sequence Alignments

RESULT 3
AAA95442
ID   AAA95442 standard; cDNA; 3280 BP.
XX
AC   AAA95442;
XX
DT   12-FEB-2001 (first entry)
XX
DE   Human CASB619 protein coding sequence #1.
XX
KW   Human; CASB619; cancer; autoimmune disease; immunogen; vaccine;
KW   epitope; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   1..3342
FT   /*tag= a
FT   /product= "CASB619"

XX
PN   WO200058460-A2.
XX
PD   05-OCT-2000.
XX
PF   20-MAR-2000; 2000WO-EP02478.
XX
PR   26-MAR-1999; 99GB-0007113.
PR   25-SEP-1999; 99GB-0022858.
XX
PA   (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI   Bruck CEM, Cassart J, Coche T, Vinals De Bassols YC;
XX
DR   WPI; 2000-664923/64.
DR   P-PSDB; AAB26179.
XX
PT   Novel CASB619 polypeptides useful for diagnosing, and as vaccines for
PT   prophylactic and therapeutic treatment of, cancers, particularly
PT   ovarian and colon carcinoma, and autoimmune diseases -
XX
PS   Claim 13; Page 53-54; 68pp; English.
XX
CC   The present sequence comprises the human CASB619 coding sequence. This
CC   protein is thought to be specifically or over-expressed in tumour cells,
CC   and so can be used as a target for antigen-specific immune responses
CC   which can cause destruction of the tumour cell. In addition, the protein
CC   and gene can be used in cancer diagnosis, in the treatment of autoimmune
CC   diseases and in vaccines against cancer and autoimmune disease. The
CC   invention provides a number of epitopes derived from the protein which
CC   can be used as immunogens.
XX
SQ   Sequence 3280 BP; 810 A; 930 C; 797 G; 743 T; 0 other;

Query Match   97.8%;   Score 3259.6;   DB 21;   Length 3280;
Best Local Similarity 99.8%;   Pred. No. 0;
Matches 3273;   Conservative   0;   Mismatches   4;   Indels   1;   Gaps   1;

Qy   58 ATGGCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGTCAGGGAAGAACTGAGAGG 117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGGCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGTCAGGGGAGAACTGAGAGG 60

Qy   118 CGCATACCCCGGCTGTGGGGCTCGTGCTCGTGGGCTCGGGACCGGCCTTCCAGGTGACCCAG 177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CGCATACCCCGGCTGTGGGGCTCGTGCTCGTGGGCTCGGGACCGGCCTTCCAGGTGACCCAG 120

Qy   178 GGAACGGGACCGGAGCTTCACGCGTCGCAAAGAGTCTGAGTACCACTATGAGTAGTACACGGCG 237
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGAACGGGACCGGAGCTTCATGCGTCGCAAAGAGTCTGAGTACCACTATGAGTAGTACACGGCG 180

Qy   238 TGTGACAGCACGGGTTCCAGGTGGGATGGGTCGCCGTGCCCGCATACCCCGGGCCTGTGCACC 297
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGTGACAGCACGGGTTCCAGGTGGGATGAGTGGGTCGCCGTGCCCGCATACCCCGGGCCTGTGCACC 240

Qy   298 AGCCTGCCTGACCCCGTCAAGGCGACCGAGTGCTCCTTCCTTCCTGCAACGCCGGGGAGTTT 357
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AGCCTGCCTGACCCCGTCAAGGGCGACCGAGTGCTCCTTCCTTCCTGCAACGCCGGGGAGTTT 300

Qy   358 CTGGATATGAAGGACCAGTCATGTAAGCACGTCATGCGTCGCCCATGCCCATGGCTTTGCCCAGCCTTTGCCCAGCCCAAC 417
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CTGGATATGAAGGACCAGTCATGTAAGCACGTCATGCGTCGCCCATGCCCATGGCTTTGCCCAGCCTTTGCCCAGCCCAAC 360

Qy   418 GGCATTCGGTTTGATGAGTGGGATGAGTGCTGCTGAGTCCACCGGAACTGTACTTCGTCCAAGTGGGTT 477
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GGCATTCGGTTTGATGAGTGGGATGAGTGCTGCTGAGTCCACCGGAACTGTACTTCGTCCAAGTGGGTT 420

Qy   478 ATGGAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTT 537
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ATGGAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTT 480

Qy   538 CCCCGGGGCGACTACAATCGCCTTCAACACGGACGAATGCACAGCCACACTGATGTAGCGCC 597
          ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db   481 CCCCGGGGCGACTACAATCGCCTTCAACACGGACGAATGCACAGCCACACTGATGTAGCGCC 540

Qy   598 GTCAACCTGCAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATC 657
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GTCAACCTGCAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATC 600

Qy   658 ATCTTTGAGTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACGAGATGACTCCAGGTGG 717
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 ATCTTTGAGTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACGAGATGACTCCAGGTGG 660

Qy   718 ATGAAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAAT 777
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 ATGAAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAAT 720

Qy   778 GTCCTCTATTGGAGACCACAGCCTTCCAGTATGGACCAAAGTACCCAAGCCTGTGCTG 837
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GTCCTCTATTGGAGACCACAGCCTTCCAGTATGGACCAAAGTACCCAAGCCTGTGCTG 780

Qy   838 GTGAGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCT 897
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GTGAGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCT 840

Qy   898 GGCACGTATGCAGCACAAGCAGGGCTCCTCTTCTGCAAACTTTGCCCAGCCAACTCTTAT 957
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GGCACGTATGCAGCACAAGCAGGGCTCCTCTTCTGCAAACTTTGCCCAGCCAACTCTTAT 900

Qy   958 TCAAATAAAGGAGAAACTTCTTGCCACCAGTGACCCTGACAAATACTCAGAGAAAGGA 1017
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 TCAAATAAAGGAGAAACTTCTTGCCACCAGTGACCCTGACAAATACTCAGAGAAAGGA 960

Qy   1018 TCTTCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACG 1077
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TCTTCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACG 1020

Qy   1078 GCCTGCGATGCCAACGGAGGAGACACAACTCATGTACAAATGGGCAAGCCGAAAATCTGT 1137
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GCCTGCGATGCCAACGGAGGAGACACAACTCATGTACAAATGGGCAAGCCGAAAATCTGT 1080

Qy   1138 AGCGAGGACCTTGAGGGGCAGTGAGTCGCTGCCTCGGTGTGGAAGACCCACTGCCCCA 1197
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AGCGAGGACCTTGAGGGGCAGTGAGTCGCTGCCTCGGTGTGGAAGACCCACTGCCCCA 1140

Qy   1198 CCCTGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGT 1257
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CCCTGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGT 1200

Qy   1258 TCCTACTCCAATGGCTTCAGACTGTTGAGTACGAGAGTCAGGGACTGAACCTGCTGTGGGA 1317
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TCCTACTCCAATGGCTTCAGACTGTTGAGTACGAGAGTCAGGGACTGAACCTGCTGTGGGA 1260

Qy   1318 TTTGAATACAAATGGTGGAACACGTGCCCACAAACATGGAAACAGCGTTCTCAGTGGG 1377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TTTGAATACAAATGGTGGAACACGTGCCCACAAACATGGAAACAGCGTTCTCAGTGGG 1320

Qy   1378 ATCAACTTCGAGTACAAGGGCATGACAGGCTGGAGTGGCTGTGATCACATTTACACA 1437
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATCAACTTCGAGTACAAGGGCATGACAGGCTGGAGTGGCTGTGATCACATTTACACA 1380

Qy   1438 GCTGCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGTTGTCCAGGATTTAGA 1497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GCTGCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGTTGTCCAGGATTTAGA 1440

Qy   1498 CCTCCGCAGTCGGTGATGGCGAGCAGACAGAATAAAGAGGTGGCCAGAATCACATTTGTC 1557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CCTCCGCAGTCGGTGATGGCGAGCAGACAGAATAAAGAGGTGGCCAGAATCACATTTGTC 1500

Qy   1558 TTTGAGACCCTCGTTCTGTGAGCTCTACTTCGTCCAAGTGGGTTGGTGTGAATTCTAGG 1617
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TTTGAGACCCTCGTTCTGTGAGCTCTACTTCGTCCAAGTGGGTTGGTGTGAATTCTAGG 1560

Qy   1618 ACCAACACTCCTGTGGAGACCTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATC 1677
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 ACCAACACTCCTGTGGAGACCTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATC 1620

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Qy  1678  ATTGAGGAGAAACTACCACGAGCTTCACCTGGCCTTCCAGAGGACCACTTTCATGAG  1737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  ATTGAGGAGAAACTACCACGAGCTTCACCTGGCCTTCCAGAGGACCACTTTCATGAG  1680

Qy  1738  GCAAGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTT  1797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681  GCAAGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTT  1740

Qy  1798  ATGAATGGCGTGGCCTCCTACTGCGTCCCTGCCCTGCCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCC  1857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  ATGAATGGCGTGGCCTCCTACTGCGTCCCTGCCCTGCCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCC  1800

Qy  1858  TCCTGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCC  1917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  TCCTGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCC  1860

Qy  1918  TGCCCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGCCTGTGCCC  1977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  TGCCCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGCCTGTGCCC  1920

Qy  1978  TGTGGTCAGGGACCAAGAACACAAGAGATCCACTCTCTGTGCTACAATGATTGCACCTTC  2037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  TGTGGTCAGGGACCAAGAACACAAGAGATCCACTCTCTGTGCTACAATGATTGCACCTTC  1980

Qy  2038  TCACGCAACACTCCAACCAGGACTTCAACTACAACTTCAACTCTCCCGCTTGGCAAACACCGTC  2097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  TCACGCAACACTCCAACCAGGACTTCAACTACAACTTCAACTCTCCCGCTTTGGCAAACACCGTC  2040

Qy  2098  ACTCTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACC  2157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  ACTCTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACC  2100

Qy  2158  CTCAGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGAC  2217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  CTCAGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGAC  2160

Qy  2218  CTCCGGATTCCTGAGGGTGAGTCAGGGTTCTCAAATCTATCACAGCCTACGTCTGCCAG  2277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  CTCCGGATTCCTGAGGGTGAGTCAGGGTTCTCAAATCTATCACAGCCTACGTCTGCCAG  2220

Qy  2278  GCAGTCATCATCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTC  2337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  GCAGTCATCATCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTC  2280

Qy  2338  AGCCTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCC  2397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  AGCCTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCC  2340

Qy  2398  CCAGCTGAACTTTTCCACCTGGAGTTCCTGTGGAATACCGGACGTGATCTTCTTTTATAGG  2457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  CCAGCTGAACTTTTCCACCTGGAGTTCCTGTGGAATACCGGACGTGATCTTCTTTTATAGG  2400

Qy  2458  TCCAATGATGTGACCCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGC  2517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  TCCAATGATGTGACCCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGC  2460

Qy  2518  AGTCCACAGAAAAACTGTCCCTGGAAGTTTGCTGCTGGAGACGTGCTCAGATGGGACC  2577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  AGTCCACAGAAAAACTGTCCCTGGAAGTTTGCTGCTGGAGACGTGCTCAGATGGGACC  2520

Qy  2578  TGTGATGGCTGCAACTTGCAACTTCCACCTCCGAGTCTCTGTGGGAGAGCGCGCTGCCCGGCTCTGCTCA  2637
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  TGTGATGGCTGCAACTTGCAACTTCCACCTCCGAGTCTCTGTGGGAGAGCGCGCTGCCCGGCTCTGCTCA  2580

Qy  2638  GTGGCTGACTACCAGTCCTATCGTCAGCAGCTGTGTGGCTGTGTGGCTGGCTGTGTGCTGGAGACTACTTAC  2697
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  GTGGCTGACTACCAGTCCTATCGTCAGCAGCTGTGTGGCTGTGTGGCTGGCTGTGTGCTGGAGACTACTTAC  2640

Qy  2698  GTGTGGCGAGAACCCAAGCTTATGCTCTGGTGGCCATTTCTCTGCCTGCAGCAGAGTCACC  2757
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  GTGTGGCGAGAACCCAAGCTTATGCTCTGGTGGCCATTTCTCTGCCTGCAGCAGAGTCACC  2700

Qy  2758  ATCTGCAAAACCATAGATTTCTGGCTGACCTGTCCATCTTCGCTGAAAGTGGGCATCTCGCAGGCACCTGTACTGCC  2817


Db  2701  ATCTGCAAAACCATAGATTTCTGGCTGACCTGTCCATCTTCGCTGAAAGTGGGCATCTCGCAGGCACCTGTACTGCC  2760

Qy  2818  ATCCTGCTCACCGTCTCACCGTCTTGACCTGCTCACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAG  2877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  ATCCTGCTCACCGTCTCACCGTCTTGACCTGCTCACTTTTGGAAAAAAGAATCAAAAACTAGAGTACAAG  2820

Qy  2878  TACTCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGCGACAGC  2937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  TACTCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGCGACAGC  2880

Qy  2938  TGGGCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAA-TCA  2996
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db  2881  TGGGCCATCATGGAAGGCGAGGATGTGAGAGGACGACCTCATCTTTACCAGCAAGAGTCA  2940

Qy  2997  CTCTTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTG  3056
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  CTCTTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTG  3000

Qy  3057  CCGGCTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCA  3116
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  CCGGCTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCA  3060

Qy  3117  CCTGCCTCCTCACCTTGCATAGCCACCTTTGCAAGCCTGCGGCGGCGGATTTGGGTGCCAGCATC  3176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  CCTGCCTCCTCACCTTGCATAGCCACCTTTGCAAGCCTGCGGCGGCGGATTTGGGTGCCAGCATC  3120

Qy  3177  CTGCAACACCCACTGCTGGAAATCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAG  3236
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  CTGCAACACCCACTGCTGGAAATCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAG  3180

Qy  3237  ATCTTTTTTATAGAGTACCCCAAACCCTCCTTTCTGCTTGCTGCTTGCTTCTGCCAAATATA  3296
          ||||||||||||||||||||||||||||||||||   |||||||||||||||||||||||
Db  3181  ATCTTTTTTATAGAGTACCCCAAACCCTCCTTTCTGCTTGCTTCTGCCAAATATA  3240

Qy  3297  CCCACACTTTGTTTGTTGTAAATTAAAAAAAAAAAAAAA  3334
          ||||||||||||||||||| |||||||||||||||
Db  3241  CCCACACTTTGTTTGTTTGTAAAAAAAAAAAAAAAAAAAA  3278
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RESULT 2
AAB26179
ID   AAB26179 standard; Protein; 1013 AA.
XX
AC   AAB26179;
XX
DT   12-FEB-2001 (first entry)
XX
DE   Human CASB619 protein #1.
XX
KW   Human; CASB619; cancer; autoimmune disease; immunogen; vaccine;
KW   epitope.
XX
OS   Homo sapiens.
XX
PN   WO200058460-A2.
XX
PD   05-OCT-2000.
XX
PF   20-MAR-2000; 2000WO-EP02478.
XX
PR   26-MAR-1999; 99GB-0007113.
PR   25-SEP-1999; 99GB-0022858.
XX
PA   (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI   Bruck CEM, Cassart J, Coche T, Vinals De Bassols YC;
XX
DR   WPI; 2000-664923/64.
DR   N-PSDB; AAA95442.
XX
PT   Novel CASB619 polypeptides useful for diagnosing, and as vaccines for
PT   prophylactic and therapeutic treatment of, cancers, particularly
PT   ovarian and colon carcinoma, and autoimmune diseases
XX
PS   Claim 4; Page 54-56; 68pp; English.
XX
CC   The present sequence comprises the human CASB619 protein sequence. This
CC   protein is thought to be specifically or over-expressed in tumour cells,
CC   and so can be used as a target for antigen-specific immune responses
CC   which can cause destruction of the tumour cell. In addition, the protein
CC   and gene can be used in cancer diagnosis, in the treatment of autoimmune
CC   diseases and in vaccines against cancer and autoimmune disease. The
CC   invention provides a number of epitopes derived from the protein which
CC   can be used as immunogens.
XX
SQ   Sequence   1013 AA;

Query Match   97.6%; Score 5376; DB 21; Length 1013;
Best Local Similarity   99.4%; Pred. No. 0;
Matches 978; Conservative   1; Mismatches   1; Indels   5; Gaps   0;

Qy   1 MAEPGHSHHLSARVRGRTERRIPRLMRLLLWAGTAFQVTQGTGPELHACKESEYHYEYTA 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MAEPGHSHHLSARVRGRTERRIPRLMRLLLWAGTAFQVTQGTGPELHACKESEYHYEYTA 60

Qy   61 CDSTGSRWRVAVPHTPGLCTSLPDPVKGTECSFSCNAGEFLDMKDQSCKPCAEGRYSLGT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CDSTGSRWRVAVPHTPGLCTSLPDPVKGTECSFSCNAGEFLDMKDQSCKPCAEGRYSLGT 120

Qy   121 GIRFDEWDELPHGFASLSANMELDDSAAESTGNCTSSKWVPRGDYIAFNTDECTATLMYA 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GIRFDEWDELPHGFASLSANMELDDSAAESTGNCTSSKWVPRGDYIASNTDECTATLMYA 180

Qy   181 VNLKQSGTVNFEYYYPDSSIIFEFFVQNDQCQPNADDSRWMKTTEKGWEFHSVELNRGNN 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VNLKQSGTVNFEYYYPDSSIIFEFFVQNDQCQPNADDSRWMKTTEKGWEFHSVELNRGNN 240

Qy   241 VLYWRTTAFSVWTKVPKPVLVRNIAITGVAYTSECFPCKPGTYADKQGSSFCKLCPANSY 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 VLYWRTTAFSVWTKVPKPVLVRNIAITGVAYTSECFPCKPGTYADKQGSSFCKLCPANSY 300

Qy   301 SNKGETSCHQCDPDKYSEKGSSSCNVRPACTDKDYFYTHTACDANGETQLMYKWAKPKIC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 SNKGETSCHQCDPDKYSEKGSSSCNVRPACTDKDYFYTHTACDANGETQLMYKWAKPKIC 360

Qy   361 SEDLEGAVKLPASGVKTHCPPCNPGFFKTNNSTCQPCPYGSYSNGSDCTRCPAGTEPAVG 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 SEDLEGAVKLPASGVKTHCPPCNPGFFKTNNSTCQPCPYGSYSNGSDCTRCPAGTEPAVG 420

Qy   421 FEYKWWNTLPTNMETTVLSGINFEYKGMTGWEVAGDHIYTAAGASDNDFMILTLVVPGFR 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 FEYKWWNTLPTNMETTVLSGINFEYKGMTGWEVAGDHIYTAAGASDNDFMILTLVVPGFR 480

Qy   481 PPQSVMADTENKEVARITFVFETLCSVNCELYFMVGVNSRTNTPVETWKGSKGKQSYTYI 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 PPQSVMADTENKEVARITFVFETLCSVNCELYFMVGVNSRTNTPVETWKGSKGKQSYTYI 540

Qy   541 IEENTTTSFTWAFQRTTFHEASRKYTNDVAKIYSINVTNVMNGVASYCRPCALEASDVGS 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 IEENTTTSFTWAFQRTTFHEASRKYTNDVAKIYSINVTNVMNGVASYCRPCALEASDVGS 600

Qy   601 SCTSCPAGYYIDRDSGTCHSCPPNTILKAHQPYGQACVPCGPGTKNNKIHSLCYNDCTF 660
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Db   601 SCTSCPAGYYIDRDSGTCHSCPPNTILKAHQPYGQACVPCGPGTKNNKIHSLCYNDCTF 660

Qy   661 SRNTPTRTFNYNFSALANTVTLAGGPSFTSKGLKYFHHFTLSLCGNQGRKMSVCTDNVTD 720
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Db   661 SRNTPTRTFNYNFSALANTVTLAGGPSFTSKGLKYFHHFTLSLCGNQGRKMSVCTDNVTD 720

Qy   721 LRIPEGESGFSKSITAYVCQAVIIPPEVTGYKAGVSSQPVSLADRLIGVTTDMTLDGITS 780
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Qy   781 PAELFHLESLGIPDVIFFYRSNDVTQSCSSGRSTTIRVRCSPQKTVPGSLLLPGTCSDGT 840
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Qy   841 CDGCNFHFLWESAAACPLCSVADYHAIVSSCVAGIQKTTYVWREPKLCSGGISLPEQRVT 900
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Qy   901 ICKTIDFWLKVGISAGTCTAILLTVLTCYFWKKNQKLEYKYSKLVMNATLKDCDLPAADS 960
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Db   901 ICKTIDFWLKVGISAGTCTAILLTVLTCYFWKKNQKLEYKYSKLVMNATLKDCDLPAADS 960

Qy   961 CAIMEGEDVEDDLIFTSKNHSLGR 984
           ||||||||||||||||||| :
Db   961 CAIMEGEDVEDDLIFTSKKSLFGK 984

us-10-046-433-40.oligo.ral

RESULT 1
US-08-190-029A-10
; Sequence 10, Application US/08190029A
; Patent No. 5736363
GENERAL INFORMATION:
  APPLICANT: EDWARDS, Richard Mark
  APPLICANT: BAWDEN, Lindsey
  TITLE OF INVENTION: IGF-II ANALOGUES
  NUMBER OF SEQUENCES: 12
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
    STREET: 10 S. WACKER DRIVE, SUITE 3000
    CITY: CHICAGO
    STATE: ILLINOIS
    COUNTRY: U.S.A.
    ZIP: 60606
  ~~ABLE FORM:
  ~~ppy disk
  FILING FORM:
PRIOR APP~
APP~ APP~

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/190,029A
  FILING DATE: 28-FEB-1994
  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/GB92/01389
  FILING DATE: 27-JUL-1992
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: GB 9202401.7
  FILING DATE: 05-FEB-1992
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: GB 9116325.3
  FILING DATE: 29-JUL-1991
ATTORNEY/AGENT INFORMATION:
  NAME: JOHN J. MCDONNELL
  REGISTRATION NUMBER: 26,949
  REFERENCE/DOCKET NUMBER: 94,062
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 312-715-1000
  TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
  LENGTH: 349 amino acids
  TYPE: amino acid
  TOPOLOGY: linear
  MOLECULE TYPE: protein
US-08-190-029A-10

Query Match   0.8%; Score 8; DB 1; Length 349;
Best Local Similarity 100.0%; Pred. No. 10;
Matches   8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy. 680 VTLAGGPS 687
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Db   110 VTLAGGPS 117

RESULT 2
US-08-462-695-10
; Sequence 10, Application US/08462695
; Patent No. 5854025
  GENERAL INFORMATION:
  APPLICANT: EDWARDS, Richard Mark
  APPLICANT: BAWDEN, Lindsey
  TITLE OF INVENTION: IGF-II ANALOGUES
  NUMBER OF SEQUENCES: 12
  CORRESPONDENCE ADDRESS: BANNER & ALLEGRETTI, LTD.
    ADDRESSEE: BANNER & ALLEGRETTI, LTD.
    STREET: 10 S. WACKER DRIVE, SUITE 3000
    CITY: CHICAGO
    STATE: ILLINOIS
    COUNTRY: U.S.A.
    ZIP: 60606
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/462,695
  FILING DATE: 5-JUN-1995
  CLASSIFICATION: .435
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/190,029
  FILING DATE: 28-FEB-1994
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: PCT/GB92/01389
  FILING DATE: 27-JUL-1992
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: GB 9202401.7

ALIGNMENTS

#			Sequence	Patent
101	6	0.6	282	1	Sequence 19, Appl	US-08-318-947A-19
102	6	0.6	282	2	Sequence 19, App	US-08-795-303-19
103	6	0.6	282	4	Sequence 222, App	US-09-071-035-222
104	6	0.6	286	4	Sequence 176, App	US-09-071-035-176
105	6	0.6	293	4	Sequence 5333, Ap	US-09-134-001C-5333
106	6	0.6	305	4	Sequence 5038, Ap	US-09-134-001C-5038
107	6	0.6	305	4	Sequence 174, App	US-09-071-035-174
108	6	0.6	314	4	Sequence 15, Appl	US-09-215-252-15
109	6	0.6	317	4	Sequence 27, Appl	US-08-118-270-27
110	6	0.6	317	5	Sequence 27, Appl	PCT-US93-08528-27
111	6	0.6	318	4	Sequence 32, Appl	US-09-068-051A-32
112	6	0.6	324	2	Sequence 29, Appl	US-08-793-410-29
113	6	0.6	327	1	Sequence 30, Appl	US-08-793-410-30
114	6	0.6	328	1	Sequence 1, Appli	US-07-867-105B-1
115	6	0.6	328	2	Sequence 6, Appli	US-08-651-818A-2
116	6	0.6	328	2	Sequence 7, Appli	US-08-793-410-7
117	6	0.6	328	2	Sequence 2, Appli	US-09-184-826-2
118	6	0.6	328	4	Sequence 4, Appli	US-09-080-205-4
119	6	0.6	328	4	Sequence 48, Appl	US-08-853-659A-48
120	6	0.6	333	2	Sequence 4, Appli	US-08-356-180-4
121	6	0.6	341	4	Sequence 13, Appl	US-09-006-353A-13
122	6	0.6	349	4	Sequence 13, Appl	US-09-573-986-13
123	6	0.6	350	4	Sequence 1, Appli	US-09-157-603-1
124	6	0.6	350	4	Sequence 1, Appli	US-09-587-436-1
125	6	0.6	350	4	Sequence 1, Appli	US-08-927-165A-1
126	6	0.6	352	4	Sequence 1, Appli	US-09-576-160B-1
127	6	0.6	352	4	Sequence 2, Appli	US-09-576-160B-2
128	6	0.6	353	1	Sequence 2, Appli	US-08-229-418-2
129	6	0.6	353	2	Sequence 2, Appli	US-08-932-761A-2
130	6	0.6	353	2	Sequence 2, Appli	US-09-307-912-2
131	6	0.6	353	5	Sequence 2, Appli	PCT-US95-04464-2
132	6	0.6	354	4	Sequence 211, App	US-09-068-569-2
133	6	0.6	358	4	Sequence 4760, Ap	US-09-288-143-211
134	6	0.6	359	4	Sequence 36, Appl	US-09-134-001C-4760
135	6	0.6	361	2	Sequence 3, Appli	US-08-415-751-36
136	6	0.6	365	4	Sequence 2, Appli	US-08-979-424-3
137	6	0.6	365	4	Sequence 23, Appl	US-08-928-383B-2
138	6	0.6	365	4	Sequence 24, Appl	US-08-928-383B-23
139	6	0.6	365	4	Sequence 26, Appl	US-08-928-383B-24
140	6	0.6	365	4	Sequence 26, Appl	US-08-928-383B-26
141	6	0.6	365	2	Sequence 50, Appl	US-09-272-496-2
142	6	0.6	366	1	Sequence 2, Appli	US-08-554-612C-50
143	6	0.6	366	1	Sequence 2, Appli	US-08-416-756A-2
144	6	0.6	369	4	Sequence 13, Appl	US-08-880-865-2
145	6	0.6	369	4	Sequence 375, App	US-09-215-252-13
146	6	0.6	376	4	Sequence 375, App	US-08-637-759B-375
147	6	0.6	384	2	Sequence 375, App	US-08-871-355A-375
148	6	0.6	384	3	Sequence 13, Appl	US-09-201-945-375
149	6	0.6	384	4	Sequence 13, Appl	US-08-605-106-13
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RESULT 1
AAF28030
ID   AAF28030 standard; DNA; 3334 BP.
XX
AC   AAF28030;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Human TR13 receptor coding sequence SEQ ID NO: 39.
XX
KW   Human; tumour necrosis factor receptor; TR13; TR14; infection;
KW   cancer; autoimmune disease; allergy; inflammatory disease;
KW   graft rejection; apoptosis; cardiovascular disease; aneurysm; ds.
XX
OS   Homo sapiens.
XX
PN   WO200105834-A1.
XX
PD   25-JAN-2001.
XX
PF   14-JUL-2000; 2000WO-US19343.
XX
PR   16-JUL-1999;   99US-0144087.
PR   18-AUG-1999;   99US-0149450.
PR   20-AUG-1999;   99US-0149712.
PR   10-SEP-1999;   99US-0153089.
XX
PA   (HUMA-). HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Ni J, Young PE;
XX
DR   WPI; 2001-112682/12.
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XX
PT   Nucleic acids encoding 2 human tumor necrosis factor receptor
PT   polypeptides ((TR13) and (TR14)), useful for the prevention, diagnosis
PT   and treatment of, e.g. cancers, acquired immune deficiency syndrome and
PT   hypohidrotic ectodermal dysplasia -
XX
PS   Claim 4; Page 394-398; 418pp; English.
XX
CC   The present invention provides the protein and coding sequences of the
CC   human tumour necrosis factor receptors TR13 and TR14. These sequences are
CC   useful in the diagnosis and treatment of many diseases, including cancer,
CC   autoimmune diseases, cardiovascular disorders, allergies,
CC   neurodegenerative diseases, graft rejection, inflammation, aneurysms and
CC   infections.
XX
SQ   Sequence 3334 BP; 820 A; 952 C; 811 G; 751 T; 0 other;

Query Match    100.0%;   Score 3334;   DB 22;   Length 3334;
Best Local Similarity    100.0%;   Pred. No. 0;
Matches 3334;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;
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Qy     1  GCGAGAAGCAGCAGCCGCAGCCACCTGAGCCGCTACTGCGCCTCACTCAGGACACGCTATG  60
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Db     1  GCGAGAAGCAGCAGCCGCAGCCACCTGAGCCGCTACTGCGCCTCACTCAGGACACGCTATG  60

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Qy   121  ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGACCGCCTTCCAGTGACCCCAGGGA  180
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Qy   181  ACGGGACCGGAGCTTCACGGTTCAAGAGTCTGAGTACCACTATGAGTGCACGGCGTGT  240
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Qy   241  GACAGCACGGGTTCCAGGTGGAGGTCGCCGTGCGCCGCATACCCGGGCCTGTGCACCAGC  300
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Qy   301  CTGCCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCGCCGGGAGTTTCTG  360
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Qy   361  GATATGAAGGACCAGTCATGTCATGGGATGAGCGCCATGGCCATGGCGCTACTCCCTCGGCAGCAGGC  420
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Qy   421  ATTCGGTTTGATGAGTGGGATGAGCTGCCCCAGCCGTTGCCAGCCTCTCAGCCAACATG  480
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Db   421  ATTCGGTTTGATGAGTGGGATGAGCTGCCCCAGCCGTTGCCAGCCTCTCAGCCAACATG  480

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Db   481  GAGCTGGATGACAGTGCTGCTGTCGAGTCACCGGAACGTGTACTTCGTCGTCCAAGTGGGTTCCC  540

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Db   541  CGGGGGCGACTACATCGCTCCGCACCGGACGAATGCCACAGCCGCCACTGATGTACGGCCGTC  600

Qy   601  AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTATCCAGACTCCAGCATCATC  660
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Db   601  AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTATCCAGACTCCAGCATCATC  660

Qy   661  TTTGAGTTTTCGTTCAGAAGGACCAGTGCCAGCCCCAATGCGAGATGACTCCAGGTGATG  720
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Db   661  TTTGAGTTTTCGTTCAGAAATGACCAGTGCCAGCCCCAATGCGAGATGACTCCAGGTGATG  720

Qy   721  AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATGCAATAATGTC  780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   781  CTCTATTGGAGAACCACCAGCCTTCAGTAGTGATGGACAAAGTACCCAGCCGTGTGCTGGTG  840

Qy   841  AGAAACATTGCCATAACAGGGTGGCCTACACTTCAGAATGCTTCCCTGCAAACCTGGC  900
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Db   841  AGAAACATTGCCATAACAGGGTGGCCTACACTTCAGAATGCTTCCCTGCAAACCTGGC  900

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Db  1021  TCTTCCTGTAACGTGCGCCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC  1080

Qy  1081  TGGGATGCCAACGGAGAGACACAACTCATGTACAAATGGCCAAGCCGAAAATCTGTAGC  1140
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Qy  1261  TACTCCAATGGCTCAGACTGTACCCCTGCCCTGCGAGGACTGAACCTGCTGTGTGGGATTT  1320
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Db  3301  CACTTTGTTTGTAAATTAAAAAAAAAAAAAAAA                           3334
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Qy  1921  CCCCTAACAACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGCCCTGT    1980
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Db  1921  CCCCTAACAACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGCCCTGT    1980

Qy  1981  GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGCTACAAGATGATTGCACCTTCTCA  2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGCTACAAGATGATTGCACCTTCTCA  2040

Qy  2041  CGAACACTCCAACCAGGAGACTTCAACTACAACTTCTCCGCTTGGCAAACACCGTCACT   2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  CGCAACAACTCCAACCAGGAGACTTCAACTACAACTTCTCCGCTTGGCAAACACCGTCACT  2100

Qy  2101  CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGTTGAAAATACTTCCATCACTTTACCCTC  2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGTTGAAAATACTTCCATCACTTTACCCTC  2160

Qy  2161  AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGCACCGACAATGTCACTGACCTC    2220
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGCACCGACAATGTCACTGACCTC    2220

Qy  2221  CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA  2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA  2280

Qy  2281  GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCCGGGGTTCCTCACAGCCTGTCAGC  2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCCGGGGTTCCTCACAGCCTGTCAGC  2340

Qy  2341  CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGAATCACCTCCCCA   2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGAATCACCTCCCCA   2400

Qy  2401  GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC  2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC  2460

Qy  2461  AATGATGTGACCCAGTCTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT        2520
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  AATGATGTGACCCAGTCTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT        2520

Qy  2521  CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAAGTGCTCAGATGGGACCTGT   2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAAGTGCTCAGATGGGACCTGT   2580

Qy  2581  GATGGCTGCAACTTCCACTTCCTGTGGGGAGAGCGGGGCTGGATGGGGAGCTGCTCAGTG  2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  GATGGCTGCAACTTCCACTTCCTGTGGGGAGAGCGGGGCTGGATGGGGAGCTGCTCAGTG  2640

Qy  2641  GCTGACTACCAGCTATCGTCAGCAGCTGTGTGCTGGAGATCCAGAGACTACTTACGTG    2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  GCTGACTACCAGCTATCGTCAGCAGCTGTGTGCTGGAGATCCAGAGACTACTTACGTG    2700

Qy  2701  TGGCGAGACCCAAGCTATGCCTGGTGGCATTTCTCCTGCCTGAGCAGGCTCACCATC    2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  TGGCGAGACCCAAGCTATGCCTGGTGGCATTTCTCCTGCCTGAGCAGGCTCACCATC    2760

Qy  2761  TGCAAAACCATAGATTCTGGCTGAAAGTGGGCATCTCTGGGCACCTGTACTGCCATC    2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  TGCAAAACCATAGATTCTGGCTGAAAGTGGGCATCTCTGGGCACCTGTACTGCCATC    2820

Qy  2821  CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAGAATCAAAAACTAGAGTACAAGTAC  2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAGAATCAAAAACTAGAGTACAAGTAC  2880

Qy  2881  TCCAAGCTGGTGATGAATGCTACTCTCCAAGGACTGTGACCTGCCAGCTGTGACAGCTGC  2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  TCCAAGCTGGTGATGAATGCTACTCTCCAAGGACTGTGACCTGCCAGCTGTGACAGCTGC  2940

Qy  2941  GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAATCACTCT  3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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AAB35333
ID   AAB35333 standard; Protein; 1001 AA.
XX
AC   AAB35333;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Human TR13 receptor protein SEQ ID NO: 40.
XX
KW   Human; tumour necrosis factor receptor; TR13; TR14; infection;
KW   cancer; autoimmune disease; allergy; inflammatory disease;
KW   graft rejection; apoptosis; cardiovascular disease; aneurysm.
XX
OS   Homo sapiens.
XX
PN   WO200105834-A1.
XX
PD   25-JAN-2001.
XX
PF   14-JUL-2000; 2000WO-US19343.
XX
PR   16-JUL-1999;  99US-0144087.
PR   18-AUG-1999;  99US-0149450.
PR   20-AUG-1999;  99US-0149712.
PR   10-SEP-1999;  99US-0153089.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Ni J, Young PE;
XX
DR   WPI; 2001-112682/12.
XX
PT   Nucleic acids encoding 2 human tumor necrosis factor receptor
PT   polypeptides ((TR13) and (TR14), useful for the prevention, diagnosis
PT   and treatment of, e.g. cancers, acquired immune deficiency syndrome and
PT   hypohidrotic ectodermal dysplasia -
XX
PS   Claim 40; Page 398-401; 418pp; English.
XX
CC   The present invention provides the protein and coding sequences of the
CC   human tumour necrosis factor receptors TR13 and TR14. These sequences are
CC   useful in the diagnosis and treatment of many diseases, including cancer,
CC   autoimmune diseases, cardiovascular disorders, allergies,
CC   neurodegenerative diseases, graft rejection, inflammation, aneurysms and
CC   infections.
XX
SQ   Sequence   1001 AA;

Query Match         100.0%;   Score 1001;   DB 22;   Length 1001;
Best Local Similarity  100.0%;   Pred. No. 0;
Matches 1001;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy    1 MAEPGHSHHLSARVRGRTERRIPRLWRLLIWAGTAFQVTCGTGPELHACKESEYHYEYTA 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MAEPGHSHHLSARVRGRTERRIPRLWRLLIWAGTAFQVTCGTGPELHACKESEYHYEYTA 60

Qy   61 CDSTGSRWRVAVPHTPGLCTSLPDPVKGTECSFSCNAGEFLDMKDQSCKPCAEGRYSLGT 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CDSTGSRWRVAVPHTPGLCTSLPDPVKGTECSFSCNAGEFLDMKDQSCKPCAEGRYSLGT 120

Qy  121 GIRPDEWDELPHGFASLSANMELDDSAAESTGNCTSSKWVPRGDYIAFNTDECTATLMYA 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GIRPDEWDELPHGFASLSANMELDDSAAESTGNCTSSKWVPRGDYIAFNTDECTATLMYA 180

Qy  181 VNLKQSGTVNFEYYYPDSSIIFEFFVQNDQCQPNADDSRWMKTTEKGWEFHSVELNRGNN 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 VNLKQSGTVNFEYYYPDSSIIFEFFVQNDQCQPNADDSRWMKTTEKGWEFHSVELNRGNN 240

Qy  241 VLYWRTTAFSVWTKVPKPVLVRNIAITGVAYTSECFPCKPGTYADKQGSSPCKLCPANSY 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 VLYWRTTAFSVWTKVPKPVLVRNIAITGVAYTSECFPCKPGTYADKQGSSPCKLCPANSY 300

Qy  301 SNKGETSCHQCDPDKYSEKGSSSCNVRPACTDKDYFYTHTACDANGETQLMYKWAKPKIC 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 SNKGETSCHQCDPDKYSEKGSSSCNVRPACTDKDYFYTHTACDANGETQLMYKWAKPKIC 360

Qy  361 SEDLEGAVKLPASGVKTHCPCPNPGFPKTNNSTCQPCPYGSYSNGSDCTRCPAGTEPAVG 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 SEDLEGAVKLPASGVKTHCPCPNPGFPKTNNSTCQPCPYGSYSNGSDCTRCPAGTEPAVG 420

Qy  421 FEYKWNTLPTNMETTVLSGINFEYKGMTGWEVAGDHIYTAAGASDNDFMILTLVVPGFR 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 FEYKWNTLPTNMETTVLSGINFEYKGMTGWEVAGDHIYTAAGASDNDFMILTLVVPGFR 480

Qy  481 PPQSVMADTENKEVARITPVFETLCSVNCELYFMVGVNSRTNTPVETWKGSKGKQSYTYI 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 PPQSVMADTENKEVARITPVFETLCSVNCELYFMVGVNSRTNTPVETWKGSKGKQSYTYI 540

Qy  541 IBENTTTSFTWAFQRTTFHEASRKYTNDVAKIYSINVTNVMNGVASYCRPCALEASDVGS 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 IBENTTTSFTWAFQRTTFHEASRKYTNDVAKIYSINVTNVMNGVASYCRPCALEASDVGS 600

Qy  601 SCTSCPAGYYIDRDSGTCHSCPPNTILKAHQPYGVQACVPCGPGTKNNKIHSLCYNDCTF 660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 SCTSCPAGYYIDRDSGTCHSCPPNTILKAHQPYGVQACVPCGPGTKNNKIHSLCYNDCTF 660

Qy  661 SRNTPTRTFNYNFSALANTVTLAGGPSFTSKGLKYFHHFTLSLCGNQGRKMSVCTDNVTD 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 SRNTPTRTFNYNFSALANTVTLAGGPSFTSKGLKYFHHFTLSLCGNQGRKMSVCTDNVTD 720

Qy  721 LRIPEGESGFSKSITAYVCQAVIIPPEVTGYKAGVSSQPVSLADRLIGVTTDMTLDGITS 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 LRIPEGESGFSKSITAYVCQAVIIPPEVTGYKAGVSSQPVSLADRLIGVTTDMTLDGITS 780

Qy  781 PAELFHLBSLGIPDVIFPYRSNDVTQSCSSGRSTTIRVRCSPQKTVPGSLLLPGTCSDGT 840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 PAELFHLBSLGIPDVIFPYRSNDVTQSCSSGRSTTIRVRCSPQKTVPGSLLLPGTCSDGT 840

Qy  841 CDGCNFHFLWESAAACPLCSVADYHAIVSSCVAGIQKTTYVWREPKLCSGGISLPEQRVT 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 CDGCNFHFLWESAAACPLCSVADYHAIVSSCVAGIQKTTYVWREPKLCSGGISLPEQRVT 900

Qy  901 ICKTIDFWLKVGISAGTCTAILLLVLTCYFWKKNQKLEYKYSKLVMNATLKDCDLPAADS 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 ICKTIDFWLKVGISAGTCTAILLLVLTCYFWKKNQKLEYKYSKLVMNATLKDCDLPAADS 960

Qy  961 CAIMEGEDVEDDLLIFTSKNHSLGRSNHLPPRGLLMDLTQCR 1001
         ||||||||||||||||||||||||||||||||||||||||||
Db  961 CAIMEGEDVEDDLLIFTSKNHSLGRSNHLPPRGLLMDLTQCR 1001
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